PAGE: 1

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#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/557,8234 GENTER 1600/2800

DATE: 07/25/2000 TIME: 02:08:06

INPUT SET: S35718.raw

### This Raw Listing contains the General Information Section and up to the first 5 pages.

```
SEQUENCE LISTING
 1
 2
 3
     (1)
            General Information:
 4
 5
          (i) APPLICANTS: Bucala, Richard J. et al.
 6
 7
         (ii) TITLE OF INVENTION: Inhibition of Migration Inhibitory Factor in the Treat
 8
                 Cytokine-Mediated Toxicity
 9
10
        (iii) NUMBER OF SEQUENCES: 17
11
         (iv) CORRESPONDENCE ADDRESS:
12
               (A) ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
13
14
               (B) STREET: 2600 Century Square, 1501 Fourth Avenue
15
               (C) CITY: Seattle
               (D) STATE: WA
16
               (E) COUNTRY: U.S.A.
17
18
               (F) ZIP: 98101-1688
19
20
          (v) COMPUTER READABLE FORM:
21
               (A) MEDIUM TYPE: Floppy disk
22
               (B) COMPUTER: IBM PC compatible
23
               (C) OPERATING SYSTEM: Windows95
24
               (D) SOFTWARE: Word
25
         (vi) CURRENT APPLICATION DATA:
26
27
               (A) APPLICATION NUMBER: to be assigned
28
               (B) FILING DATE: 24 April 2000
29
               (C) CLASSIFICATION:
30
31
       (viii) ATTORNEY/AGENT INFORMATION:
32
               (A) NAME: Oster, Jeffrey B.
               (B) REGISTRATION NUMBER: 32,585
33
34
               (C) REFERENCE/DOCKET NUMBER: 0203H
35
         (ix) TELECOMMUNICATION INFORMATION:
36
37
               (A) TELEPHONE: 206 628-7711
38
               (B) TELEFAX: 206 628-7699
39
40
41
    (2) INFORMATION FOR SEQ ID NO:1:
42
          (i) SEQUENCE CHARACTERISTICS:
43
44
               (A) LENGTH: 348 base pairs
45
               (B) TYPE: nucleic acid
```

(C) STRANDEDNESS: single

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PAGE: 2

## RAW SEQUENCE LISTING PATENT APPLICATION US/09/557,823 TECH CENTER 1600/2900 TIME: 02:08:06

DATE: 07/25/2000

INPUT SET: S35718.raw

47 48	(D) TOPOLOGY: unknown											
49	(ii) MOLECULE TYPE: DNA											
50												
51	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:											
52	ARGGGRANGE MAARGGRAAA GAGAAAAN GAGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	60										
53 54	ATGCCTATGT TCATCGTGAA CACCAATGTT CCCCGCGCCT CCGTGCCAGA GGGGTTTCTG	60										
55	TCGGAGCTCA CCCAGCAGCT GGCGCAGGCC ACCGGCAAGC CCGCACAGTA CATCGCAGTG	120										
56												
57	CACGTGGTCC CGGACCAGCT CATGACTTTT AGCGGCACGA ACGATCCCTG CGCCCTCTGC	180										
58												
59	AGCCTGCACA GCATCGGCAA GATCGGTGGT GCCCAGAACC GCAACTACAG TAAGCTGCTG	240										
60 61	TGTGGCCTGC TGTCCGATCG CCTGCACATC AGCCCGGACC GGGTCTACAT CAACTATTAC	300										
62	Total Total Control Control Accordance Control	500										
63	GACATGAACG CTGCCAACGT GGGCTGGAAC GGTTCCACCT TCGCTTGA	348										
64												
65	(2) THEODY MICH FOR GEO TO NO. 2.											
66 67	(2) INFORMATION FOR SEQ ID NO:2:											
68	(i) SEQUENCE CHARACTERISTICS:											
69	(A) LENGTH: 348 base pairs											
70	(B) TYPE: nucleic acid											
71	(C) STRANDEDNESS: single											
72	(D) TOPOLOGY: unknown											
73												
74	(ii) MOLECULE TYPE: DNA											
75 76	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:											
77	(XI) SEQUENCE DESCRIPTION. SEQ ID NO.2.											
78	ATGCCGATGT TCATCGTAAA CACCAACGTG CCCCGCGCCT CCGTGCCGGA CGGGTTCCTC	60										
79												
80	TCCGAGCTCA CCCAGCAGCT GGCGCAGGCC ACCGGCAAGC CCCCCCAGTA CATCGCGGTG	120										
81		100										
82 83	CACGTGGTCC CGGACCAGCT CATGGCCTTC GGCGGCTCCA GCGAGCCGTG CGCGCTCTGC	180										
84	AGCCTGCACA GCATCGGCAA GATCGGCGGC GCGCAGAACC GCTCCTACAG CAAGCTGCTG	240										
85												
86	TGCGGCCTGC TGGCCGAGCG CCTGCGCATC AGCCCGGACA GGGTCTACAT CAACTATTAC	300										
87												
88	GACATGAACG CGGCCAGTGT GGGCTGGAAC AACTCCACCT TCGCCTAA	348										
89 90												
91	(2) INFORMATION FOR SEQ ID NO:3:											
92	(2) INIONIMIZON FOR DEG ID NO. 3.											
93	(i) SEQUENCE CHARACTERISTICS:											
94	(A) LENGTH: 501 base pairs											
95	(B) TYPE: nucleic acid											
96	(C) STRANDEDNESS: single											
97	(D) TOPOLOGY: unknown											
98	(AAA) MOLEGULE WIDE											
99	(ii) MOLECULE TYPE: cDNA											

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/557,823 TECH CENTER 1600/2800

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													IIV	PUIS	EI: 3	33/18	.raw
100										_							
101	(xi)	SEQ	UENC.	E DE:	SCRI	PTIO	N: S	EQ I	D NO	:3:							
102	aa maaam	. m . a	mma s	maama	7 33.	a	3 3 M/A	mma	aaaa	777	amaa	amaa	a. a	2000	ammm	-	60
103	CCATGCCT	AT G	TTCA	TCGT	AA د	CACC	AATG	TTC		JGC	CTCC	GTGC	CA G	AGGG	31111	_	60
104 105	TGTCGGAG	מידי מ	N C C C	አርሮእር	י כיתו	aaca	מאממ	CCA	ccaa	אגרי	geee	ממאמי	אני ייי	አ (ግ አ ጥ/	ממטאי	2	120
105	TGTCGGAG	CI C	ACCC.	MGCA	3 CI	GGCG	CAGG	CCA	CCGG	CAA	GCCC	GCAC	MG I.	ACA I	CGCA	3	120
107	TGCACGTG	מידי כי	ccaa.	ልሮሮልር	<b>з</b> Ст	ሮልሞር	<b>ል</b> ሮጥጥ	מידים.	מרממו	מאכי	CAAC	СВТС	יר די	מרמרי	ייכוזיכיי	יי	180
108	TOCACOTO	01 0		noon		On I O		1111		ono	onno	on: 0.		0000		•	100
109	GCAGCCTG	CA C	AGCA'	TCGG	CAA	GATC	GGTG	GTG	CCCA	AAE	CCGC.	AACT	AC A	GTAA	GCTG	c	240
110	•																
111	TGTGTGGC	CT G	CTGT	CCGA	r cg	CCTG	CACA	TCA	GCCC	GGA	CCGC	TCCT	AC A	GCAA	GCTG	C	300
112																	
113	TGTGCGGC	CT G	CTGG	CCGA	G CG	CCTG	CGCA	TCA	GCCC	GGA	CCGG	GTCT	AC A	TCAA	CTAT'	r	360
114																	
115	ACGACATG	AA C	GCTG	CCAA	C GT	GGGC'	TGGA	ACG	GTTC	CAC	CAGG	GTCT	AC A	TCAA	CTAT'	r	420
116																	
117	ACGACATG	AA C	GCGG	CCAG'	r gr	GGGC'	TGGA	ACA.	ACTC	CAC	CTTC	GCTT	GA G	TCCT	GGCC	C	480
118																	
119	CACTTACC	rg C	ACCG	CTGT.	r c												501
120																	
121 122	(2) INFO	יש אום	TON 1	EUD 6	בבי	או חד	0.4.										
123	(2) INFO	KMA I	LON	ron .	JEQ .	TD IN	0.1.										
124	(i)	SEO	UENC	E CHA	ARAC	TERI:	STIC	S:									
125	ζ-/	_		NGTH:					S								
126				PE: a													
127		•	•					le									
128	(C) STRANDEDNESS: single (D) TOPOLOGY: unknown																
129																	
130	(ii)	MOL	ECULI	E TYI	PE: ]	pept:	ide										
131																	
132	(xi)	SEQ	UENC	E DES	SCRI	PTIO	N: S	EQ I	D NO	: 4 :							
133		_					_	_,	_	1	_			_			
134		Pro	Met	Phe		Val	Asn	Thr	Asn		Pro	Arg	АТа	ser		Pro	
135	1				5					10					15		
136 137	<b>a</b> 1	a1	Dho	T 011	Cor	<b>a</b> 1	T 011	mb r	al n	Gl n	Leu	. דג	Cl n	. ד ג	Th r	C117	
137	GIU	СТУ	Pile	20	261	GIU	ьеu	1111	25	GIII	neu	ATG	GIII	30	1111	GLY	
139				20					23					30			
140	T.vs	Pro	Δla	Gln	Tur	Tle	Δla	Val	His	Val	Val	Pro	Asp	Gln	Leu	Met	
141	2,5		35	· · · ·	- 1 -			40					45				
142																	
143	Thr	Phe	Ser	Gly	Thr	Asn	Asp	Pro	Cys	Ala	Leu	Cys	Ser	Leu	His	Ser	
144		50		-			55		•			60					
145																	
146	Ile	Gly	Lys	Ile	Gly.	Gly	Ala	Gln	Asn	Arg	Asn	Tyr	Ser	Lys	Leu	Leu	
147	65	=	=		-	70				_	75	-				80	
148																	
149	Cys	Gly	Leu	Leu		Asp	Arg	Leu	His		Ser	Pro	Asp	Arg		Tyr	
150					85					90					95		
151	_	_	_	_	_		_						_	_		_	
152	Ile	Asn	Tyr	Tyr	Asp	Met	Asn	Ala	Ala	Asn	Val	Gly	Trp	Asn	Gly	Ser	

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### RAW SEQUENCE LISTING PATENT APPLICATION US/09/557,823

DATE: 07/25/2000 TIME: 02:08:07

INPUT SET: S35718.raw Thr Phe Ala (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 115 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro Asp Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly Lys Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met Ala Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu Cys Cly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser Thr Phe Ala (2) INFORMATION FOR SEQ ID NO:6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 9 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: peptide



#### RAW SEQUENCE LISTING PAGE: 5 PATENT APPLICATION US/09/557, 822th CENTER 1600/2900

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DATE: 07/25/2000 TIME: 02:08:07

INPUT SET: S35718.raw

```
206
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
207
208
           Ala Lys Lys Gly Ala Val Gly Gly Ile
209
           1
210
211
      (2) INFORMATION FOR SEQ ID NO:7:
212
213
214
           (i) SEQUENCE CHARACTERISTICS:
215
                (A) LENGTH: 17 amino acids
                (B) TYPE: amino acid
216
217
                (C) STRANDEDNESS: single
218
                (D) TOPOLOGY: unknown
219
          (ii) MOLECULE TYPE: peptide
220
221
222
          (ix) FEATURE:
                (A) NAME/KEY: Peptide
223
                (B) LOCATION: 15
224
225
                (D) OTHER INFORMATION: /label= X
226
                       /note= "X = Asn or Gly"
227
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
228
229
           Ile Xaa His Asn Thr Val Ala Thr Glu Ile Ser Gly Tyr Asn Xaa Ala
230
231
                           5
                                                 10
232
233
          Met
234
235
236
      (2) INFORMATION FOR SEQ ID NO:8:
237
238
           (i) SEQUENCE CHARACTERISTICS:
239
                (A) LENGTH: 27 base pairs
240
                (B) TYPE: nucleic acid
241
                (C) STRANDEDNESS: single
242
                (D) TOPOLOGY: unknown
243
244
          (ii) MOLECULE TYPE: DNA
245
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
246
247
248
     CCATATGCCG ATGTTCATCG TAAACAC
                                                                                27
249
250
251
      (2) INFORMATION FOR SEQ ID NO:9:
252
253
           (i) SEQUENCE CHARACTERISTICS:
254
                (A) LENGTH: 26 base pairs
255
                (B) TYPE: nucleic acid
256
                (C) STRANDEDNESS: single
257
               (D) TOPOLOGY: unknown
```

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## **SEQUENCE VERIFICATION REPORT** PATENT APPLICATION *US/09/557,823*

DATE: 07/25/2000 TIME: 02:08:07

INPUT SET: S35718.raw

Line

Error

Original Text

27

Wrong application Serial Number

(A) APPLICATION NUMBER: to be assigned